

Application No.: 09/745,965

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1. (currently amended) A computer implemented method for selecting nucleic acid probes comprising:  
inputting quality scores and locations for a plurality ( $n$ ) of candidate probes;  
selecting  $k$  number of probes from the  $n$  number of candidate probes, wherein the selected probes have a maximum aggregate adjusted quality score; wherein the adjusted quality score is based upon the quality score and a penalty for the overlapping of the selected probes; and  
outputting the selected probes.
2. (previously presented) The method of Claim 1 wherein the adjusted quality score is calculated according to:  $S' = S \sqrt{\frac{l-o}{l}}$ , wherein  $S'$  is an adjusted quality score;  $S$  is the initial quality score;  $l$  is the probe length, and  $o$  is the overlap the probe has with other probes.
3. (canceled)
4. (previously presented) The method of Claim 2 wherein  $k$  is greater than 3.
5. (original) The method of Claim 4 wherein  $k$  is greater than 5.

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6. (original) The method of Claim 5 wherein  $k$  is greater than 10.
7. (original) The method of Claim 6 wherein  $k$  is greater than 15.
8. (previously presented) The method of Claim 2 wherein the selecting step comprises performing dynamic programming optimization on the  $n$  number of candidate probes to adjust their quality scores to the extent of overlap between them to obtain an optimal  $k$  number of probes with optimal aggregate adjusted quality scores.
9. (previously presented) The method of Claim 8 wherein the selecting comprises steps of:
  - calculating best adjusted quality scores ( $Score(i,t)$ ) for probe  $i$  last with  $t-1$  probes chosen before  $i$  and previous location  $j$  providing this best score ( $Last(i,k)$ );
  - determining the best adjusted quality scores for  $Score(j, k)$  to select the last probe; and
  - selecting the next probe according to  $Last$ (the probe selected, number of probes remaining to be selected); and
  - repeating the selecting step until all  $k$  probes are selected.
10. (currently amended) A system for selecting nucleic acid probes comprising:

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a processor; and

a memory coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform logical steps, wherein the logical steps include:

inputting quality scores and locations for a plurality ( $n$ ) of candidate probes;  
selecting  $k$  number of probes from the  $n$  number of candidate probes, wherein the selected probes have a maximum aggregate adjusted quality score; wherein the adjusted quality score is based upon the quality score and a penalty for the overlapping of the selected probes; and  
outputting the selected probes.

11. (original) The system of Claim 10 wherein the adjusted quality score is calculated according to:  $S' = S \sqrt{\frac{l-o}{l}}$ , wherein  $S'$  is an adjusted quality score;  $S$  is a quality score;  $l$  is the probe length,  $o$  is the overlap the probe has with other probes.
12. (canceled)
13. (previously presented) The system of Claim 11 wherein  $k$  is greater than 3.
14. (original) The system of Claim 13 wherein  $k$  is greater than 5.
15. (original) The system of Claim 14 wherein  $k$  is greater than 10.

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16. (original) The system of Claim 15 wherein  $k$  is greater than 15.
17. (previously presented) The system of Claim 16 wherein the selecting step comprises performing dynamic programming optimization on the  $n$  number of candidate probes to adjust their quality scores to the extent of overlap between them to obtain an optimal  $k$  number of probes with optimal aggregate adjusted quality scores.
18. (original) The system of Claim 17 wherein the selecting comprises steps of:
- calculating best adjusted quality scores ( $Score(i,t)$ ) for probe  $i$  last with  $t-1$  probes chosen before  $i$  and previous location  $j$  providing this best score ( $Last(i,k)$ );
  - determining the best adjusted quality scores for  $Score(j,k)$  to select the last probe; and
  - selecting the next probe according to  $Last$ (the probe selected, number of probes remain to be selected); and
  - repeating the selecting step until all  $k$  probes are selected.
19. (currently amended) A computer readable medium having computer executable instructions for performing a method comprising:
- inputting quality scores and locations for a plurality ( $n$ ) of candidate probes;

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selecting  $k$  number of probes from the  $n$  number of candidate probes,  
wherein the selected probes have a maximum aggregate adjusted quality score;  
wherein the adjusted quality score is based upon the quality score and a penalty  
for the overlapping of the selected probes; and  
outputting the selected probes.

20. (original) The computer readable medium of Claim 19 wherein the adjusted quality score is calculated according to:  $S' = S \sqrt{\frac{l-o}{l}}$ , wherein  $S'$  is an adjusted quality score;  $S$  is a quality score;  $l$  is the probe length,  $o$  is the overlap the probe has with other probes.
21. (canceled)
22. (previously presented) The computer readable medium of Claim 20 wherein  $k$  is greater than 3.
23. (original) The computer readable medium of Claim 22 wherein  $k$  is greater than 5.
24. (original) The computer readable medium of Claim 23 wherein  $k$  is greater than 10.
25. (original) The computer readable medium of Claim 24 wherein  $k$  is greater than 15.

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26. (previously presented) The computer readable medium of Claim 25 wherein the selecting step comprises performing dynamic programming optimization on the  $n$  number of candidate probes to adjust their quality scores to the extent of overlap between them to obtain an optimal  $k$  number of probes with optimal aggregate adjusted quality scores.
27. (original) The computer readable medium of Claim 26 wherein the selecting comprises steps of:
- calculating best adjusted quality scores ( $Score(i,t)$ ) for probe  $i$  last with  $t-1$  probes chosen before  $i$  and previous location  $j$  providing this best score ( $Last(i,k)$ );
  - determining the best adjusted quality scores for  $Score(j,k)$  to select the last probe; and
  - selecting the next probe according to  $Last$ (the probe selected, number of probes remain to be selected); and
  - repeating the selecting step until all  $k$  probes are selected.
28. (new) A computer implemented method for selecting nucleic acid probes comprising:
- inputting quality scores and locations for a plurality ( $n$ ) of candidate probes;
  - selecting  $k$  number of probes from the  $n$  number of candidate probes, wherein the selected probes have a maximum aggregate adjusted quality score; wherein the

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adjusted quality score is based upon the quality score and a penalty for the overlapping of the selected probes; and  
outputting the selected probes, wherein the outputting of the selected probe sequences is to a file.

29. (new) A system for selecting nucleic acid probes comprising:

a processor; and

a memory coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform logical steps, wherein the logical steps include:

inputting quality scores and locations for a plurality ( $n$ ) of candidate probes;

selecting  $k$  number of probes from the  $n$  number of candidate probes, wherein the

selected probes have a maximum aggregate adjusted quality score; wherein the

adjusted quality score is based upon the quality score and a penalty for the

overlapping of the selected probes; and

outputting the selected probes, wherein the outputting of the selected probe sequences is to a file.

30. (new) A computer readable medium having computer executable instructions for performing a method comprising:

inputting quality scores and locations for a plurality ( $n$ ) of candidate probes;

selecting  $k$  number of probes from the  $n$  number of candidate probes,

wherein the selected probes have a maximum aggregate adjusted quality score;

wherein the adjusted quality score is based upon the quality score and a penalty

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for the overlapping of the selected probes; and  
outputting the selected probes, wherein the outputting of the selected probe  
sequences is to a file.